

SEQUENCE LISTING

<110> Duvick, Jon

<120> Compositions and Methods for Fummonisin Detoxification

<130> 5718-111

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<170> PatentIn Ver. 2.0

<210> 1

<211> 1691

<212> DNA

<213> Exophiala spinifera

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<223> flavin monooxygenase with intron

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<211> 1638

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase, fully spliced cDNA

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<211> 545

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> flavin monooxygenase, translation of fully spliced
cDNA

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Leu Arg Lys Leu Arg Leu Asn Ala Lys Ile Phe Glu Gly Ala Pro Asp
35 40 45

Phe Gly Gly Val Trp His Trp Asn Arg Tyr Pro Gly Ala Arg Val Asp
50 55 60

Ser Glu Thr Pro Phe Tyr Gln Leu Asn Ile Pro Glu Val Trp Lys Asp
65 70 75 80

Trp Thr Trp Ser Cys Arg Tyr Pro Asp Gln Lys Glu Leu Leu Ser Tyr
85 90 95

Val His His Cys Asp Lys Ile Arg Gly Leu Arg Lys Asp Val Tyr Phe
100 105 110

Gly Ala Glu Val Val Asp Ala Arg Tyr Ala Arg Asp Leu Gly Thr Trp
115 120 125

Thr Val Lys Thr Ser Ala Gly His Val Ala Thr Ala Lys Tyr Leu Ile
130 135 140

Leu Ala Thr Gly Leu Leu His Arg Lys His Thr Pro Ala Leu Pro Gly
145 150 155 160

Leu Ala Asp Phe Asn Gly Lys Val Ile His Ser Ser Ala Trp His Glu
165 170 175

Asp Phe Asp Ala Glu Gly Gln Arg Val Ala Val Ile Gly Ala Gly Ala
180 185 190

Thr Ser Ile Gln Ile Val Gln Glu Leu Ala Lys Lys Ala Asp Gln Val
195 200 205

Thr Met Phe Met Arg Arg Pro Ser Tyr Cys Leu Pro Met Arg Gln Arg
210 215 220

Thr Met Asp Arg Asn Glu Gln Thr Ala Trp Lys Ala Tyr Tyr Pro Thr
225 230 235 240

Leu Phe Glu Ala Ser Arg Lys Ser Arg Ile Gly Phe Pro Val Gln Ala
245 250 255

Pro Ser Val Gly Ile Phe Glu Val Ser Pro Glu Gln Arg Glu Ala Tyr
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Phe Glu Glu Leu Trp Glu Arg Gly Ala Phe Asn Phe Leu Ala Cys Gln
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Tyr Arg Glu Val Met Val Asp Lys Lys Ala Asn Arg Leu Val Tyr Asp
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Phe Trp Ala Lys Lys Thr Arg Ser Arg Ile Val Asn Pro Ala Lys Arg
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Asp Leu Met Ala Pro Leu Glu Pro Pro Tyr Trp Phe Gly Thr Lys Arg
325 330 335

Ser Pro Leu Glu Ser Asp Tyr Tyr Glu Met Leu Asp Lys Pro Ser Val
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Glu Ile Val Asn Leu Glu Gln Ser Pro Ile Val Ala Val Thr Lys Thr
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Gly Val Leu Leu Ser Asp Gly Ser Lys Arg Glu Cys Asp Thr Ile Val
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Leu Ala Thr Gly Phe Asp Ser Phe Thr Gly Ser Leu Thr His Met Gly
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Leu Lys Asn Lys His Gly Val Asp Leu Lys Glu Val Trp Lys Asp Gly
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Ile Ser Thr Tyr Met Gly Val Phe Ser His Gly Phe Pro Asn Ala Phe
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Glu Ala Glu His Ala Thr Ser Val Glu Ala Thr Lys Ser Ala Gln Glu
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Ala Trp Ser Ile Met Ile Ala Lys Met Asn Glu His Thr Leu Phe Pro
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Cys
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<210> 4

<211> 1464

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> aldehyde dehydrogenase , fully spliced cDNA

<400> 4

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<211> 487
<212> PRT
<213> *Exophiala spinifera*

<220>
<223> aldehyde dehydrogenase, translation of fully
spliced cDNA

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35 40 45

Asp Val Asp Ser Ala Val Ala Ala Ser Val Gln Ala Val Lys Lys Gly
50 55 60

Pro Trp Lys Lys Phe Thr Gly Ala Gln Arg Ala Ala Cys Met Leu Lys
65 70 75 80

Phe Ala Asp Leu Ala Glu Lys Asn Ala Glu Lys Leu Ala Arg Leu Glu
85 90 95

Ser Leu Pro Thr Gly Arg Pro Val Ser Met Ile Thr His Phe Asp Ile
100 105 110

Pro Asn Met Val Ser Val Phe Arg Tyr Tyr Ala Gly Trp Ala Asp Lys
115 120 125

Ile Ala Gly Lys Thr Phe Pro Glu Asp Asn Gly Lys Pro Asn Trp Arg
130 135 140

Tyr Glu Pro Met Gly Val Cys Ala Gly Ile Ala Ser Trp Asn Ala Thr
145 150 155 160

Phe Leu Tyr Val Gly Trp Lys Ile Ala Pro Ala Leu Ala Ala Gly Cys
165 170 175

Ser Phe Ile Phe Lys Ala Ser Glu Lys Ser Pro Leu Gly Val Leu Gly
180 185 190

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Glu Thr Gln Thr Pro Phe Gly Gly Met Lys Gln Ser Gly Ser Gly Arg
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Glu Leu Gly Glu Glu Gly Leu Lys Ala Tyr Leu Glu Pro Lys Thr Ile
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Asn Ile His Val Asn Ile Glu
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<210> 6

<211> 1764

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> permease, partially spliced cDNA

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<211> 1578

<212> DNA

<213> *Exophiala spinifera*

<220>

<223> permease, fully spliced cDNA

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<210> 8

<211> 525

<212> PRT

<213> *Exophiala spinifera*

<220>

<223> permease, translation of fully spliced cDNA

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35 40 45

Ser Leu Ala Phe Val Ile Cys Asn Ser Trp Ala Gly Ile Ser Gly Ser
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Leu Gln Leu Ala Leu Leu Ala Gly Gly Pro Val Thr Leu Leu Tyr Gly
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Glu Leu Thr Ser Val Tyr Pro Thr Ala Gly Gly Gln Tyr His Phe Ala
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Gly Leu Val Ser Leu Leu Ser Trp Ile Ala Ile Gly Ser Ser Val Thr
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145 150 155 160

Thr Tyr Ser Gln Asp Ser Trp His Val Phe Leu Ile Tyr Glu Gly Val
165 170 175

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180 185 190

Trp Val His Glu Ile Gly Phe Gly Leu Thr Ile Ala Leu Phe Val Ile
195 200 205

Ser Phe Ile Ala Ile Leu Ala Arg Ser Asn Pro Lys Ala Pro Asn Ser
210 215 220

Gln Val Trp Thr Ala Trp Ser Asn Tyr Thr Gly Trp Ser Asp Gly Val
225 230 235 240

Cys Phe Ile Leu Gly Leu Ser Thr Ser Cys Phe Met Phe Ile Gly Leu
245 250 255

Asp	Ala	Ala	Met	His	Leu	Ala	Glu	Glu	Cys	Thr	Asp	Ala	Ala	Arg	Thr	260	265	270	
Val	Pro	Lys	Ala	Val	Val	Ser	Ala	Ile	Ile	Ile	Gly	Phe	Cys	Thr	Ala	275	280	285	
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Ile	Leu	Ser	Ser	Ala	Gly	Tyr	Ile	Pro	Phe	Glu	Thr	Met	Arg	Gln	Ser	305	310	315	320
Ala	Arg	Ile	Arg	Leu	Phe	Ala	Thr	Val	Leu	Ser	Cys	Gly	Gly	Ile	Val	325	330	335	
Met	Ala	Phe	Phe	Ala	Leu	Asn	Ala	Val	Gln	Glu	Thr	Ala	Ser	Arg	Leu	340	345	350	
Thr	Trp	Ser	Phe	Ala	Arg	Asp	Asn	Gly	Leu	Val	Phe	Ser	Thr	His	Leu	355	360	365	
Glu	Arg	Ile	His	Pro	Arg	Trp	Gln	Val	Pro	Val	Trp	Ser	Leu	Phe	Ala	370	375	380	
Thr	Trp	Gly	Ile	Leu	Ala	Thr	Cys	Gly	Cys	Ile	Phe	Leu	Gly	Ser	Ser	385	390	395	400
Thr	Ala	Phe	Asn	Ala	Leu	Val	Asn	Ser	Ala	Val	Val	Leu	Gln	Gln	Leu	405	410	415	
Ser	Phe	Leu	Ile	Pro	Ile	Ala	Leu	Leu	Leu	Tyr	Gln	Lys	Arg	Asp	Pro	420	425	430	
Lys	Phe	Leu	Pro	Ser	Thr	Arg	Ala	Phe	Val	Leu	Pro	Arg	Gly	Ile	Gly	435	440	445	
Phe	Leu	Val	Asn	Val	Leu	Ala	Val	Val	Phe	Thr	Ser	Val	Thr	Thr	Val	450	455	460	
Phe	Phe	Ser	Phe	Pro	Leu	Thr	Val	Pro	Thr	Ala	Ala	Ser	Thr	Met	Asn	465	470	475	480
Tyr	Thr	Ser	Ala	Ile	Ile	Gly	Val	Ala	Leu	Ala	Leu	Gly	Val	Leu	Asn	485	490	495	
Trp	Val	Val	His	Ala	Arg	Lys	His	Tyr	Gln	Gly	Pro	His	Leu	Glu	Leu	500	505	510	

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<211> 3999
<212> DNA
<213> *Exophiala spinifera*

<220>
<223> p-glycoprotein, with introns

<400> 9

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ggatcatttc gtectgtggt tcgtctacct ctttattggg aagtttgtcc tcacgtacgt 360
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<211> 3792

<212> DNA

<213> *Exophiala spinifera*

<220>

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<211> 1263

<212> PRT

<213> Exophiala spinifera

<220>

<223> p-glycoprotein, translation of fully spliced cDNA

<400> 11

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Ser Ser Ser His Pro Pro Pro Glu Lys Glu Thr Glu Gly Ser Ile Ser
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Asp Tyr Leu Arg Ile Phe Arg Tyr Ala Asp Lys Tyr Asp Trp Thr Leu
35 40 45

Asn Val Ile Ala Leu Ile Cys Ala Ile Gly Ser Gly Ala Ser Leu Pro
50 55 60

Leu Met Ser Ile Ile Phe Gly Ser Phe Thr Asn Lys Phe Asn Asn Tyr
65 70 75 80

Asn Ser Gly Asp Gly Ser Pro Glu Ala Phe Lys Ala Asp Val Asp His
85 90 95

Phe Val Leu Trp Phe Val Tyr Leu Phe Ile Gly Lys Phe Val Leu Thr
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Tyr Val Ser Thr Ala Ala Ile Thr Ile Ser Ala Ile Arg Thr Thr Arg
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Thr Leu Arg Arg Val Phe Leu Glu Cys Thr Leu Arg Gln Glu Val Trp
130 135 140

His Phe Asp Lys Gln Ser Asn Gly Ala Ile Ala Thr Xaa Val Thr Thr
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Asn Gly Asn Arg Ile Gln Thr Gly Ile Ala Glu Lys Leu Val Phe Thr
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Val Gln Ala Leu Ser Met Phe Phe Ser Ala Phe Val Val Ala Leu Ala
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Phe Leu Val Thr Gly Ile Cys Ile Ala Ile Asp Ala Ala Gln Glu Ala
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Arg Ile Thr Arg Ile Tyr Ser Arg Ala Ala Val Leu Ala Glu Glu Val
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Leu Ser Ser Ile Arg Thr Val His Ala Phe Tyr Ala Gln Lys Lys Met
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Val Glu Lys Tyr Asp Val Phe Leu Gln Gln Ala His Gln Glu Gly Lys
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Ile Tyr Ala Ala Ile Ala Leu Ala Phe Trp Lys Gly Phe Arg Met Tyr
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Pro Glu Gly Cys Leu Gly Gln Ile Glu Ile Gln Asn Leu Ala Phe Ala
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Tyr Pro Ser Arg Pro Ser Ala Gln Val Leu Arg Asp Phe Asn Leu Thr
385 390 395 400

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Gly	Arg	Ile	Leu	Leu	Asp	Gly	Leu	Glu	Leu	Gly	Gln	Tyr	Asn	Val	Lys	435	440	445	
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Ala	Asp	Glu	Gln	Gln	Glu	His	Glu	Lys	Thr	Leu	His	Glu	Lys	Ala	Ala	625	630	635	640
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Thr Leu Gly Tyr Ser Leu Leu Lys Cys Ile Leu Ile Met Phe Tyr Glu
675 680 685

Gln Lys Asn Leu Tyr Trp Cys Phe Leu Leu Ser Thr Ile Thr Val Leu
690 695 700

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725 730 735

Phe Tyr Ile Leu Met Phe Phe Val Val Ala Leu Gly Asn Leu Val Gly
740 745 750

Tyr Phe Thr Ile Gly Trp Thr Cys Asn Val Ile Ser Gln Val Val Thr
755 760 765

His Arg Tyr Gln Ala Ala Met Phe Gln Arg Val Leu Asp Gln Asp Ile
770 775 780

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785 790 795 800

Leu Ser Ala Leu Pro Thr Gln Leu Gln Glu Leu Ile Ser Ala Asn Phe
805 810 815

Leu Ile Tyr Ile Val Val Gly Gln His Arg Leu Glu Gln Cys Ser Thr
820 825 830

Thr Ser Leu Trp Met Glu Thr Gly Pro Gly Gly Cys Val Trp Cys Thr
835 840 845

Ser Thr Pro Ala Phe Gly Trp Leu Pro Gln Asn Ser Ser Arg Asp Glu
850 855 860

Ala Arg Ser Arg Lys Leu Gly Lys Leu Cys Arg Lys Cys Trp Ala Cys
865 870 875 880

Lys Arg Ser Ser Tyr Arg Asp Pro Asp Arg Leu Ile Phe Asp Ser Arg
885 890 895

Arg Pro Cys Ser Pro Thr Val Leu Gly His Val Glu Gln Gly Leu Ala
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Lys Ile Ile Gln Ser Phe Trp Phe Gly Arg Cys Phe Gly Phe His Leu
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Gly Cys Gly Lys Ser Thr Leu Ile Ala Leu Ser Glu Arg Phe Tyr Asp
 1060 1065 1070

Pro Thr Ser Gly Arg Ile Ser Phe Ala His Glu Asn Ile Ala Glu Met
 1075 1080 1085

Ser Pro Arg Leu Tyr Arg Gly His Met Ser Leu Val Gln Gln Glu Pro
 1090 1095 1100

Thr Leu Tyr Gln Gly Ser Val Arg Glu Asn Val Thr Leu Ala Leu Glu
 1105 1110 1115 1120

Ala Glu Leu Ser Glu Glu Leu Cys Gln Gly Arg Leu Pro Ala Arg Pro
 1125 1130 1135

Met Leu Trp Ile Leu Ser Ser Leu Tyr Gln Lys Ala Leu Lys Arg Leu
 1140 1145 1150

Ala Ala Gln Arg Gly Met Gln Phe Ser Gly Gly Gln Arg Gln Arg Ile
 1155 1160 1165

Ala Ile Ala Arg Ala Leu Ile Arg Asn Pro Lys Leu Leu Leu Leu Asp
1170 1175 1180

Glu Ala Thr Ser Ala Leu Asp Thr Gln Ser Glu Arg Leu Val Gln Ala
1185 1190 1195 1200

Ala Leu Asp Glu Ala Ser Thr Ser Arg Thr Thr Ile Ala Val Ala His
1205 1210 1215

Arg Leu Ser Thr Ile Arg Asn Val Asp Val Ile Phe Val Phe Ala Asn
1220 1225 1230

Gly Arg Ile Ala Glu Thr Gly Thr His Ala Glu Leu Gln Arg Leu Arg
1235 1240 1245

Gly Arg Tyr Tyr Glu Met Cys Leu Ala Gln Ser Leu Asp Gln Ala
1250 1255 1260

1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500